

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/069,251DATE: 03/08/2002
TIME: 03:50:03

INPUT SET: S36792.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: NAKAMURA, KAZUYASU
KOIKE, MASAMICHI
SHITARA, KENYA
HANAI, NOBUO
KUWANA, YOSHIHISA
HASEGAWA, MAMORU

(ii) TITLE OF INVENTION: HUMANIZED ANTIBODIES

(iii) NUMBER OF SEQUENCES: 113

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: NIXON & VANDERHYE P.C.
(B) STREET: 1100 NORTH GLEBE ROAD
(C) CITY: ARLINGTON
(D) STATE: VIRGINIA
(E) COUNTRY: U.S.A.
(F) ZIP: 22201-4714

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/673,799
(B) FILING DATE: 27-JUN-96
(C) CLASSIFICATION:

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703)816-4000
(B) TELEFAX: (703)816-4100

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

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47
48 (ii) MOLECULE TYPE: Other nucleic acid
49
50 (ix) FEATURE:
51 (A) NAME/KEY: sig_peptide
52 (B) LOCATION: 33..89
53 (C) IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN
54 ESTABLISHED CONSENSUS
55
56
57 (ix) FEATURE:
58 (A) NAME/KEY: domain
59 (B) LOCATION: 181..194
60 (C) IDENTIFICATION METHOD: BY SIMILARITY
61 WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
62 CONSENSUS
63 (D) OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
64
65 (ix) FEATURE:
66 (A) NAME/KEY: domain
67 (B) LOCATION: 237..284
68 (C) IDENTIFICATION METHOD: BY SIMILARITY
69 WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
70 CONSENSUS
71 (D) OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
72
73 (ix) FEATURE:
74 (A) NAME/KEY: domain
75 (B) LOCATION: 384..416
76 (C) IDENTIFICATION METHOD: BY SIMILARITY
77 WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
78 CONSENSUS
79 (D) OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
80
81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
82
83 CTCCACAGTC CCTGAAGACA CTGACTCTAA CC ATG GGA TGG AGC TGG ATC TTT 53
84 Met Gly Trp Ser Trp Ile Phe
85 -15
86
87 CTC TTC CTC CTG TCA GGA ACT GCA GGT GTC CTC TCT GAG GTC CAG CTG 101
88 Leu Phe Leu Leu Ser Gly Thr Ala Gly Val Leu Ser Glu Val Gln Leu
89 -10 -5 1
90
91 CAG CAG TCT GGA CCT GAG CTG GTG AAG CCT GGG GCT TCA GTG AAG ATA 149
92 Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile
93 5 10 15 20
94
95 TCC TGC AAG GCT TCT GGA TAC ACA TTC ACT GAC TAC AAC ATG GAC TGG 197
96 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met Asp Trp
97 25 30 35
98
99 GTG AAG CAG AGC CAT GGA AAG AGC CTT GAG TGG ATT GGA TAT ATT TAT 245

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100 Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile Tyr
101          40          45          50
102
103 CCT AAC AAT GGT GGT ACT GGC TAC AAC CAG AAG TTC AAG AGC AAG GCC      293
104 Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe Lys Ser Lys Ala
105          55          60          65
106
107 ACA TTG ACT GTA GAC AAG TCC TCC AGC ACA GCC TAC ATG GAG CTC CAC      341
108 Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu His
109          70          75          80
110
111 AGC CTG ACA TCT GAG GAC TCT GCA GTC TAT TAC TGT GCA ACC TAC GGT      389
112 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Thr Tyr Gly
113      85          90          95          100
114
115 CAT TAC TAC GGC TAC ATG TTT GCT TAC TGG GGC CAA GGG ACT CTG GTC      437
116 His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
117          105          110          115
118
119 ACT GTC TCT GCA      449
120 Thr Val Ser Ala
121          120
122
123

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: both

- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 7..72
- (C) IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN ESTABLISHED CONSENSUS

(ix) FEATURE:

- (A) NAME/KEY: domain
- (B) LOCATION: 142..170
- (C) IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED CONSENSUS
- (D) OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"

(ix) FEATURE:

- (A) NAME/KEY: domain
- (B) LOCATION: 217..237
- (C) IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED

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153             CONSENSUS
154             (D) OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
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156             (ix) FEATURE:
157                 (A) NAME/KEY: domain
158                 (B) LOCATION: 334..360
159                 (C) IDENTIFICATION METHOD: BY SIMILARITY
160                     WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
161                     CONSENSUS
162             (D) OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
163
164             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
165
166             GACAAA ATG CAT TTT CAA GTG CAG ATT TTC AGC TTC CTG CTA ATC AGT             48
167             Met His Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser
168             -20                               -15                               -10
169
170             GCC TCA GTC ATA ATG TCC AGA GGA CAA ATT GTT CTC ACC CAG TCT CCA             96
171             Ala Ser Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro
172             -5                               1                               5
173             GCA ATC ATG TCT GCA TCT CCA GGG GAG AAG GTC ACC ATA ACC TGC AGT             144
174             Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser
175             10                               15                               20
176
177             GCC AGC TCA AGT GTA AGT TAC ATG CAC TGG TTC CAG CAG AAG CCA GGC             192
178             Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly
179             25                               30                               35                               40
180
181             ACT TCT CCC AAA CTC TGG ATT TAT AGC ACA TCC AAC CTG GCT TCT GGA             240
182             Thr Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly
183             45                               50                               55
184
185             GTC CCT GCT CGC TTC AGT GGC AGT GGA TCT GGG ACC TCT TAC TCT CTC             288
186             Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
187             60                               65                               70
188
189             ACA ATC AGC CGA ATG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG             336
190             Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
191             75                               80                               85
192
193             CAA AGG AGT AGT TAC CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA             384
194             Gln Arg Ser Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
195             90                               95                               100
196
197             ATA AAA CGG             393
198             Ile Lys Arg
199             105
200
201
202             (2) INFORMATION FOR SEQ ID NO:3:
203
204             (i) SEQUENCE CHARACTERISTICS:
205                 (A) LENGTH: 443 base pairs

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206         (B) TYPE: nucleic acid
207 (C) STRANDEDNESS: both
208         (D) TOPOLOGY: linear
209         (ii) MOLECULE TYPE: Other nucleic acid
210
211         (ix) FEATURE:
212             (A) NAME/KEY: sig_peptide
213             (B) LOCATION: 34..89
214             (C) IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN
215                 ESTABLISHED CONSENSUS
216
217         (ix) FEATURE:
218             (A) NAME/KEY: domain
219             (B) LOCATION: 180..194
220             (C) IDENTIFICATION METHOD: BY SIMILARITY
221                 WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
222                 CONSENSUS
223             (D) OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
224
225         (ix) FEATURE:
226             (A) NAME/KEY: domain
227             (B) LOCATION: 252..287
228             (C) IDENTIFICATION METHOD: BY SIMILARITY
229                 WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
230                 CONSENSUS
231             (D) OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
232
233         (ix) FEATURE:
234             (A) NAME/KEY: domain
235             (B) LOCATION: 384..410
236             (C) IDENTIFICATION METHOD: BY SIMILARITY
237                 WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
238                 CONSENSUS
239             (D) OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
240
241         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
242
243         CTCCACAGTC CCTGAAGACA CTGACTCTAA CC ATG GGA TGG AGC TGG ATC TTT      53
244                                     Met Gly Trp Ser Trp Ile Phe
245                                     -15
246
247         CTC TTC CTC CTG TCA GGA ACT GCA GGT GTC CTC TCT GAG GTC CAG CTG      101
248         Leu Phe Leu Leu Ser Gly Thr Ala Gly Val Leu Ser Glu Val Gln Leu
249         -10                      -5                      1
250
251         CAG CAG TCT GGA CCT GAG CTG GTG AAG CCT GGG GCT TCA GTG AAG ATA      149
252         Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile
253         5                      10                      15                      20
254
255         TCC TGC AAG GCT TCT GGA TAC ACA TTC ACT GAC TAC AAC ATG GAC TGG      197
256         Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Asn Met Asp Trp
257         25                      30                      35
258

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
31	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/673,799

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SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/10/069,251

DATE: 03/08/2002
TIME: 03:50:04

INPUT SET: S36792.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/10/069,251

DATE: 03/08/2002
TIME: 03:50:05

INPUT SET: S36792.raw

Line	Original Text	Corrected Text
528	(C) STRANDEDNES: both	(C) STRANDEDNESS: both